



Sequence Listing

(1) GENERAL INFORMATION:

(i) APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.

(ii) TITLE OF INVENTION: Inducing Apoptosis Using Anti-Apo-2 Antibodies

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US/10/052,798A
(B) FILING DATE: 02-NOV-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/079029
(B) FILING DATE: 14-MAY-1998

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/046615
(B) FILING DATE: 15-MAY-1997

(ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/074119
(B) FILING DATE: 09-FEB-1998

(x) ATTORNEY/AGENT INFORMATION:
(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1101R2D1

(xi) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-5416
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
185 190 195

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp
215 220 225

Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
230 235 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
 305 310 315
 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
 320 325 330
 Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
 335 340 345
 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
 350 355 360
 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
 365 370 375
 Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
 380 385 390
 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405
 Ala Asp Ser Ala Xaa Ser
 410

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC CGCATAAATC AGCACGGGC CGGAGAACCC CGCAATCTCT 50
 GCGCCCACAA AATACACCGA CGATGCCGA TCTACTTTAA GGGCTGAAAC 100
 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
 Met Glu
 1
 CAA CGG GGA CAG AAC GCC CCG GCT TCG GGG GCC CGG 184
 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 5 10 15
 AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
 20 25
 AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
 Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
 30 35 40
 GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
 Val Ala Ala Val Leu Leu Val Ser Ala Glu Ser Ala
 45 50
 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
 Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
 55 60 65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 70 75 80

 TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
 85 90

 TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
 95 100 105

 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
 Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
 110 115

 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACC ACG ACC 535
 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
 120 125 130

 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
 135 140 145

 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
 150 155

 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
 160 165 170

 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
 175 180

 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
 185 190 195

 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
 200 205 210

 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
 215 220

 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
 Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
 225 230 235

 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
 Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
 240 245

 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
 Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
 250 255 260

 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
 Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
 265 270 275

CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
 Pro Gly Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 280 285

GAA AGG TCT CAG AGG AGG CTG CTG GTT CCA GCA AAT 1042
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
 290 295 300

GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
 305 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
 315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Gly His Arg Asp Thr Leu
 345 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411

CCTTCCCTGG TTTACCTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTCAC AGCACCTTT TATCCTAACATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 930 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
30 35

GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA 153
Ala Glu Val Gln Leu Val Gln Ser Gly Gly Val Glu

40

45

50

CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
 Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg
 65 70 75

CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
 80 85 90

AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309
 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
 95 100

AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
 Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn
 105 110 115

TCC CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA 426
 Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly
 130 135 140

CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG 465
 Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr
 145 150 155

GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT 504
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 160 165

GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC 543
 Gly Ser Gly Gly Ser Ser Glu Leu Thr Gln Asp
 170 175 180

CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC 582
 Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile
 185 190

ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC 621
 Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 195 200 205

TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC 660
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
 210 215 220

ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC 699
 Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
 225 230

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
 Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu
 235 240 245

ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777

Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	
													250
													255
TAC	TGT	AAC	TCC	CGG	GAC	AGC	AGT	GGT	AAC	CAT	GTG	GTA	816
Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His	Val	Val	
260				265									270
TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	GGT	GCG	GCC	855
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala	
275							280						285
GCA	CAT	CAT	CAT	CAC	CAT	CAC	GGG	GCC	GCA	GAA	CAA	AAA	894
Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	
290								295					
CTC	ATC	TCA	GAA	GAG	GAT	CTG	AAT	GGG	GCC	GCA	TAG	930	
Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala			
300						305							309

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 939 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	ACC	ATG	ATT	ACG	CCA	AGC	TTT	GGA	GCC	TTT	TTT	36	
Met		Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	
1				5								10	
TTG	GAG	ATT	TTC	AAC	GTG	AAA	AAA	TTA	TTA	TTC	GCA	ATT	75
Leu	Glu	Ile	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	
15						20						25	
CCT	TTA	GTT	GTT	CCT	TTC	TAT	GCG	GCC	CAG	CCG	GCC	ATG	114
Pro	Leu	Val	Val	Pro	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	
30							35						
GCC	GGG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	153
Ala	Gly	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	
40						45						50	
CAG	CCT	GGG	GGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	192
Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
55						60							
GGA	TTC	ACC	TTT	AGT	AGC	TAT	TGG	ATG	AGC	TGG	GTC	CGC	231
Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser	Trp	Val	Arg	
65						70						75	
CAG	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTG	GCC	AAC	ATA	270
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	
80						85						90	
AAG	CAA	GAT	GGA	AGT	GAG	AAA	TAC	TAT	GTG	GAC	TCT	GTG	309
Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	
95												100	
AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 105 110 115
 TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125
 ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val
 130 135 140
 AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465
 Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg
 145 150 155
 GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 160 165
 GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543
 Gly Gly Gly Ser Gly Gly Gly Ser Ser Glu Leu
 170 175 180
 ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582
 Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
 185 190
 GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621
 Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
 195 200 205
 TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660
 Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 210 215 220
 GTA CTT GTC ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG 699
 Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
 225 230
 ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738
 Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr
 235 240 245
 GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777
 Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
 250 255
 GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816
 Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
 260 265 270
 CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
 His Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 275 280 285
 GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894
 Gly Ala Ala Ala His His His His His His Gly Ala Ala
 290 295
 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
 300 305 310

GCA TAG 939

A1a
312

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	ACC	ATG	ATT	ACG	CCA	AGC	TTT	GGA	GCC	TTT	TTT	36	
Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe		
1		5					10						
TTG	GAG	ATT	TTC	AAC	GTG	AAA	AAA	TTA	TTA	TTC	GCA	ATT	75
Leu	Glu	Ile	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	
15			20					25					
CCT	TTA	GTT	GTT	CCT	TTC	TAT	GCG	GCC	CAG	CCG	GCC	ATG	114
Pro	Leu	Val	Val	Pro	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	
	30						35						
GCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGC	GTG	GTC	153
Ala	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	
40			45					50					
CAG	CCT	GGG	CGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCT	TCT	192
Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
	55				60								
GGG	TTC	ATT	TTC	AGT	AGT	TAT	GGG	ATG	CAC	TGG	GTC	CGC	231
Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	
65			70				75						
CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	GCA	GGT	ATT	270
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile	
80			85					90					
TTT	TAT	GAT	GGA	GGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	GTG	309
Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	95					100							
AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	348
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
105			110				115						
ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC	387
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
	120				125								
ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	AGG	GGC	TAC	TAC	426
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	
130			135				140						
TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	465
Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
145				150				155					

TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504
Ser Ser Gly Gly Ser Gly Gly Ser Gly 160 165

GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543
Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser 170 175 180

GTC TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582
Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys 185 190

ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621
Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val 195 200 205

CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660
His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu 210 215 220

CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699
Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro 225 230

GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738
Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser 235 240 245

CTG GCC ATC ACT GGG CTC CAG GCT GAA GAT GAG GCT GAT 777
Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp 250 255

TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGG GGT TCG 816
Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg Gly Ser 260 265 270

GTA TTC GGC GGA GGG ACC AAG GTC ACT GTC CTA GGT GCG 855
Val Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala 275 280 285

GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA 894
Ala Ala His His His His His Gly Ala Ala Glu Gln 290 295

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala 300 305 310

TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro

20	25	30												
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Gln	Leu	Val	Gln
				35					40					45
Ser	Gly	Gly	Gly	Val	Glu	Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser
				50					55					60
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp
					65				70					75
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile
				80					85					90
Asn	Trp	Asn	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	Lys	Gly
					95				100					105
Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
				110					115					120
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				125					130					135
Ala	Lys	Ile	Leu	Gly	Ala	Gly	Arg	Gly	Trp	Tyr	Phe	Asp	Leu	Trp
				140					145					150
Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
				155					160					165
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Ser	Glu	Leu	Thr	Gln	
				170					175					180
Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	Arg	Ile	Thr
				185					190					195
Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	Trp	Tyr	Gln
				200					205					210
Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	Gly	Lys	Asn
				215					220					225
Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser
				230					235					240
Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp
				245					250					255
Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His
				260					265					270
Val	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala	
				275					280					285
Ala	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	
				290					295					300
Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala						
				305										

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
20 25 30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu
35 40 45

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
50 55 60

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp
65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
80 85 90

Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
125 130 135

Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe
140 145 150

Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly
155 160 165

Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Glu
170 175 180

Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
185 190 195

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
200 205 210

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
215 220 225

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
230 235 240

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
245 250 255

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser
260 265 270

Gly Asn His Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu
275 280 285

Gly Ala Ala Ala His His His His His Gly Ala Ala Glu Gln

290

295

300

Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 305 310

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: Amino Acid
 - (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile
1				5					10					15
Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro
					20					25				30
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln
				35					40					45
Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser
				50					55					60
Cys	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp
					65				70					75
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile
				80					85					90
Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
				95					100					105
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu
				110					115					120
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				125					130					135
Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly
				140					145					150
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
				155					160					165
Gly	Ser	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	
				170					175					180
Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr
				185					190					195
Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	His	Trp	Tyr
				200					205					210
Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Asp
				215					220					225
Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg
				230					235					240
Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu

245	250	255
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg		
260	265	270
Gly Ser Val Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala		
275	280	285
Ala Ala His His His His Gly Ala Ala Glu Gln Lys Leu		
290	295	300
Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala		
305	310	

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCGGATAAC AATTCACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGACGGTAG T 21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
1 5 10 15

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
20 25 30

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
35 40 45

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
50 55 60

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
65 70 75

Asp

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met Arg
1 5 10 15

Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly
20 25 30

Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp
35 40 45

Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp
50 55 60

Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln
65 70 75

Asp

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
1 5 10 15

Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu
20 25 30

Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp
35 40 45

Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu
50 55 60

Glu Arg Met Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser
65 70

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg
1 5 10 15

Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln
20 25 30

Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr
35 40 45

Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu
50 55 60

Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp
65 70 75

Ile Glu Glu

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg
1 5 10 15

Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp
20 25 30

Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn
35 40 45

Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile
50 55 60

Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
65 70 75

Gln Thr